

FIG.2A

```
RSTHGANIDPTFFLSRTVSNVISSIVFGDRFDYKDKEFLSLLRMMLGIFQFTSTSTGQ CLYEMFSSVMKHLPGPQQQAFQLLQGLEDFIAKKVEHNQRTLDPNSPRDFIDSFLIRMQ 6
                                                                                                                                                                                                                                                                                                                                                                                      IGKNRQPKFEDRAKMPYMEAVIHEIQRFGDVIPMSLARRVKKDTKFRDFFLPKGIEVF
                                                                                                                                                                                                                                                                                                                                                                                                                     PMLGSVLRDLRFFSNPRDFNPQHFLGEKGQFKKRDAFVPFSIRKRNCFGEGLARMELF
                                                                                                                                                                                                                                   NYLQLNTEQMYNSLMKISERYGPVFTIHLGPRRVVVLCGHDAVREALVDOAEEFSGRG
                                                                                                                                                                                                                                                                  EQATFDWVFKGYGVVFSNGERAKQLLRFAIATLRDFGVGKRGIEERIQEESGFLIEAI
                                                                                                                                                                                                                                                                                                                                                         EEEKNPNTEFYLKNLMMSTLNLFIAGTETVSTTLGYGFLLLMKHPEVEAKVHEEIDRV
                                                                                                                                                                                                        /translation=MLASGMLLVALLACLTVMVLMSVWQQRKSKGKLPPGPTPLPFIG
                                                        6308..6489)
                             2499..2659
                                                      ..4398,4873..5060,5577..5718,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFFTTVMQNFRLKSSQSPKDIDVSPKHVGFATIPRNYTMSFLPR
                          2115..2264,
                             (791..970, 1237..1399,
                                                                                                                                             product=cytochrome P450"
                                                                                                                                                                        db_xref-PID:g1008462"
                                                                                    gene=CYP2A6V2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene=CYP2A6V2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene=CYP2A6V2:
                                                                                                                codon start=1
                                                       3207..3383,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1237..1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2115..2264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     791..970
5'UTR
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
```

ORIGIN

																			Ţ
																			1627
																			g
	A6V2:			A6V2:			A6V2:			A6V2:			A6V2:			A6V2:			1746
/number=3 24992659	gene=CYP2	number=4	2073383	gene=CYP2	number=5	2564398	gene=CYP2	number=6	8735060	gene=CYP2	number=7	5775718	gene=CYP2	number=8	63086489	gene=CYP2	number=9	4906744	2196 c
7	_	`	~	_	_	4	\	_	Ţ	_	_	Ŋ	_	_	_	_	_	9	Ø
																			1646
exon			exon			exon			exon			exon			exon			3'UTR	BASE COUNT

5/59

FIG.2A CONT. BASE COUNT

							•														
gatggcagtg	tctgggcatc	ctgggctgct	aaactccaca	ggaatcccc	cacagccaca	acccccagat	caagtgctcc	ctcctaaatc	ccctctctg	ctaggcagga	agccaaagtc	tctatcatcc	gcctgactgt	ctccgggacc	tgtacaactc	tgcctagttg	aatggagttt	ctgtgagaac	agagtggagg	tggccccgtg	tgccgtcagg
caatgaagaa	caatgaggat	ggacccagtg	ctcctcccag	ccatatgcct	cccctaaatg	ctcccctgga	atccaaagcc	ctgttgccc	gtctggaggc	gtgtcccaag	ttatgtaatc	gccgtcacca	ttgctggcct	gggaagctgc	acagagcaga	gggtgggggc	agtcttagga	agctccctga	ggccccattc	gtgagcgcta	gtggacatga
ctccccttgc	tctgaggttc	gtcagcccct	ctacacactc	actttcaagt	caacagaaga	ttggattcct	cagaccccaa	tacagcttat	cacagattta	cttgctggct	aatgaggtaa	aaccacccca	tctggtggcc	gaagagcaag	gcagctgaac	gggtgtctcg	tgtggaccaġ	tgggatgtcc	ctcggtgctg	catcagatca	gtggtgctgt
tctggtcttc	ctggcctcac	gctaaatcaa	gctgggcttg	tagccccgag	gcatcctcca	acccagacct	ttctcactct	tcctcagttc	cctgaagtac	cttatcctcc	tgggaggtga	tataaaggca	cagggatgct	ggcagcagag	gaaactacct	acagggagat	ggttgaccag	gacaggatct	cacatgacat	cacccacctc	ccggcgggtc
gaaatatggc	ggcagccatc	tctgggcaaa	ggagaacgcc	tgggtcttcc	ccttaaccct	ccctaataaa	ttggggtgca	tattccaaac	cggcacccct	ctggggtccc	ggcatgtagt	tttcaggcag	atgctggcct	atgtctgttt	cccttcattg	gtgtcccaag	tgtggcaggg	gcatcagaaa	agcatcccag	taaccactcc	acttggggcc
aagttcccct	gaggttctat	aagagacagc	gggctttctg	cccacagccc	ttcctgagac	ctttgtctta	ccgcacaact	cctatgcaaa	cacagccctg	\circ	ttcatggtgg	catccctct	ctctaccacc	gatggtcttg	caccccattg	cctcatgaag	gctggggctt	tggagtttca	ctgggtgcga	gttctccctc	ttcaccattc
↔	61	121	∞	241	0	9	421	481	541	601	661	721	781	841	901	961	1021	1081	1141	1201	1261

1321 gaggetetgg tggaccagge tgaggagtte agegggegag gegageaage caeettegae

ט ט	,,		, ,	,		, ma	<i>r</i>	<i>T</i> \				ι	ಹ	<i>(</i>)	75	g	7		Ø	Ö	Ö
cacgaaggtc	gtc	tccctcacct	ccttattctc	tgggtttctg	ttctgggctt	taggatgcca	ctcttccttc	cttaagaatc	cccaccctcc	atccaatgga	ctgggtaata	tcctgcgctt	agcgcatcca	aggggaccc	gttctgcctg	tggcgctgg	ctctgagttg	atcccacctt	accgctttga	tccagttcac	ttaccaaaa
gcaggtgga	aggataa	tccatgtgta	tgccccacct	ctccatctct	ccctcttagc	tcctctgtct	gtaacagtct	tccagctcag	atctcactac	tgcggacgcg	ctggccgtac	gccaagcagc	ggcatcgagg	cacggtgagc	acccgcgcgc	ccctggagtc	ctcctcagac	gccaatatcg	gtctttgggg	ctaggaatct	gtgaaggccc
agcagaaggtg ggggaaggtg	tgacaact	ttggggcctc	tgactatata	teceetetet	gtctttgagg	tctcaattct	ccatctcctg	aactctctgc	atctccccat	cccactgccc	atctctctgt	cggggagcgc	gggcaagcga	ccggagcacg	aggacgagga	gcacttccag	aattctgact	acccggaggc	cagctccatt	gcgcatgatg	agcccggccc
tgaccaagag tgaccaagag	tgactct	tctccctaca	gattcctccc	teceetetet	gtctacatga	cggatccctt	tcttcaggct	ctcaatatta	ctccacccag	tctttctctc	agctatgtgc	tattcagcaa	acttcggggt	tcgaggccat	gaaaacaccc	aaaggcgccc	tgcctcctgg	ctcccgacat	ccaatgtcat	tgtcactgtt	taatggttgc
lygallayyl aaggetatgg	ccttc	tccctcccca	gccctgtcct	gtctcctctt	ctgggtctct	ctcatctctc	tacttccaca	ctgtttctat	agaggatgtc	tccatcactc	aatgccgtga	ctaggcgtgg	accctgaggg	ggcttcctca	gcaggagaag	ctaggtgggg	aacaaggccc	caaccccctt	cgcacagtct	aaagagttcc	acggggcagg
gaggicicigg tgggtcttca	ಹ	agtctggtct	tctccagc	tctcactgga	tttaccagcc	ctctgggttt	gggttattcc	cagaccctct	tcacaccaag	atcctctgcc	gtgtggagct	acctgatcga	tgccatcgcc	ggaggagtcg	gtgcggg	g	aatttggctc	actctctccc	cttcctgagc	ctataaggac	gtcaacctcc
ى ر	1441	50	56	62	68	74	80	86	92	98	04	10	16	22	28	34	40	46	52	58	2641

gattgcttga taagaaaaa gtcagcaagg ctgtaatccc gaccagcctg catggtggcg gtctgggtga attcaaatta ttcatagcca ttcattgact atgcaaagcc tgtccttccc atgaaacacc gattagttcc tcagttcctt aagggctgg gctcccaaa ggcacgtgtt ttcttgaata gtgagcctg ccccggacag agacccggg caagtcagta cggacagatg taaaaagtaa gagtcagggc ggctaacagc aggagttcga attagttggg ttgcactcca gaggctggag acacaggccc tgcctttaac ccgtgacagc gctggaggac cccacgggac ctgcggggag ctcttcggtg tacccaggtc aaactttaga teccaeegee gagtggaacc cacaacagat tctcaccctg tgataattga gcaacgccag tcaggaggct gatcacggca atcacttgtt ttagcaagac tgggtgccgt acctgaggtc aaatccaaaa ccagcagcca caggcagatg tgctgcaagg atcccaattc agctcagctc ggagaccaga agctcctgcc ggccccaaat caaattggca accgggatag agatgctcc atgagatgt ccttcctgt ctccagctac cctgtgcaac acagctaagt agcattgggg aaaaaatta caggtggatc tctctactaa aatgagccaa cgcacgctgg gaggtacacc gggagtgggg cacaattggc gcctttcagt gggtacctaa cctaaccacc cattcccatc cccagctct ggggaaggg ctccagggac gcataccctc aatttctaac ccgatttggg gagaaggaag cagaggttgc gcatgtgcag tggcgtccgg aaaaagctg ccctgtgtca aaatcagtct taataatcct gaggccgagg tcaaaccccg ctctctgcaa gcagcaacag gcacaaccag ccgcatgcag aaacaaatcc ctctgaaata ttcccctacc aaatcagtcc atcccctgct acttaccggt cggaaaccct ctggcaggat taacgaaggt atggtcatgc gctcaggagt aaaaacaaa cgaagggggg cagaatgagg ttcccatcct agaaggtgga aggcagaggg acctcatca agcactttgg gccaacatgg tgccaggacc ccttctcat tatccggccc ccttgctatg acagagcctg cccatcccca tttaacacc cggcaaattg tgtcccctca tggttgtcca 961 3781 841 901 3661 3181 3241 3301 3241 3481 3541 3601 3061 3361 3001 941

8/59

gtctcccaaa	tggaccccat	tagaaggaca	aactcctgcc	aggtcccca	cagaaatctc	34
gtcataggga	tcggccttt	ccctttccat	aacagaagcc	tatcttaaga	ccaaacttcc	
acacatgttc	ggagaatcaa	ctttgtgtca	tctccagact	gtcctgcatc	acactcctga	22
ttccacttag	cgttccacct	ccaccacatc	acttccccaa	gtcaaaaaag	ccctcaatca	16
ctgtcccact	tttctagacc	cattagaagc	atcccaccca	tgtccccagc	ccctctctg	10
gggactccag	ccagactacg	cccccaccc	gtgctatccg	cctccctaag	gggatttctt	04
accaagtttc	caaaaaggac	cccgcagagt	atgagtttgg	cgtgatcccc	ggag	98
gagatccaaa	agtgatccac	acatggaggc	aagatgccct	ggaccgggcc	ccaagtttga	92
aaccggcagc	gatcggcaag	ttgacagagt	catgaggaga	agccaaggtc	ctcctcccc	86
cacattcccc	gatacctaaa	gagaccccta	ttcctgctct	ggactatcat	ttgcctatcc	80
ccaccccatt	ggcatttcat	cataggcgga	acttccgtct	tgaatgctct	gttctgt	74
gggtgatgtc	caatgcgaat	cctactccaa	ttaacaggat	cacaacctgg	gtgattctgg	68
tgcctcccct	ttcctccctg	atcccctaag	ccaccgggtc	actgcccgtt	ctgagtgccc	62
cccaagccca	tcacttctgt	gattggtcag	tgtctgcact	atattgaaaa	agatattaaa	56
gagtctcatt	ggcatcagct	tcagctggta	agggcaacat	gtccagagac	gtgacttgct	50
accctgagac	agatcccggg	cacctgtccc	gcaatgtccc	ttcgactggt	aaaattcccc	4 4
ccagaccctc	gtggagggcc	ggggacggaa	aaggctggag	ggtggagggt	agcacccaga	38
ctgctcatga	tggcttctta	ccctgcacta	gtcagcacca	caccgagacg	tcattgcagg	32
ttgaacctct	gatgagcacg	agaacctgat	ttctacttga	caacacggag	agaagaaccc	26
cttcaggagg	cccctctcc	tgtcctaaag	ggagtgaggt	aggtcaagca	tggtgccctg	20
aacccctaga	ccatggggtg	agtggaagat	tgaacctaag	cccattggtc	cctcttgacc	14
cttggggtcc	ctgtgtagat	agactcgagt	ggattgcgct	gagggtgctg	aagagaggtc	08
tcttgcccca	caccctgcgg	ccctcttctc	gatctagggc	agtctggtag	tcctagagcg	\circ

aagagtagta	ttatgctatg	aacccttaca	agaggaagga	agctgggatg	ggtgcttccg	99
accttgataa	ggctcagttc	aaacagaagc	ggaagagaag	gtggctagag	aaggggc	09
ggcggaaagg	cag	gctaagactg	gagggcgca	gggcttggga	g	54
gaaagggcag	cggggccagg	gtctggtggg	gccggtgaag	cgagggctgt	ccccgctgag	6481
gagcttcctg	actacaccat	atcccacgaa	ctttgccacg	aacacgtggg	gtgtccccca	42
ggacattgac	agtcacctaa	aagtcctccc	cttccgcctc	tcatgcagaa	ttcaccaccg	36
cttctcttc	gaatggagct	ggcctggcca	tttcggagaa	agcggaactg	tcctcaggaa	30
ccgcctctcc	tccacccctc	gggcttcacc	cactgagagt	ggcgaggctg	teggtactgg	24
cagctggagg	gggagagccg	cttcctccct	atattccacc	tcagggccat	¥	18
aggctccctc	gagggtcaag	tgaggtcaag	tcaaggaaac	tttgggtcac	ttggtcatct	12
accccatctt	gcatcgatca	tggacacctg	cctcccattg	ggatcttaaa	gggggaagg	90
gttcttatct	atatttggga	acagcaggtc	agatgacggc	cctaaaaagg	cttcagcatc	00
acaggagatt	ctagggtcac	atttatttcc	agaatcagag	aaggccagag	g	94
tcagaggcgg	catacccctt	aaggaaacat	ggcaaaagga	cctgtgccca	gcacc	88
taactaccaa	gatactccct	gccaccaggt	ctaccgtcga	tgttagcaat	ggcaagttcc	82
tccccagctt	gcctagtatt	ctgccgtgta	gttcccctct	cccttaccca	gcaggggcc	9 /
actcacacca	caggcttact	tgtttggtgc	aagagaccac	ctccatcagt	ىد	70
cgtgatgctt	gtttaagaag	agaaggggca	ttcctgggtg	tccccagcac	gggacttcaa	64
tccaacccc	caggttcttc	tgagagacct	ggctccgtgc	ccctatgttg	tagaagtgtt	58
tcccagggca	tactactaca	acatacacct	ccgcctcatc	atcccccaac	actctcaaca	52
gcccctgtgt	tececeteca	gcaccctagt	cctcaccggg	tgccacttcc	ttcccatgcc	46
aggtccccaa	cctccctcag	cccccaaggt	aaccttctat	cagagatgtg	cttcctgtt	5401

cagataaggc acatacaggg ctgtccgggg gcccacactc cccattttac taagtgccca aaaagcacc caaaaaccat tgcttgctac ggcgttcatg tcacaaaaca acagattett ctgaacatcc ctgcacacat acatgactgg cacctttgtt gtgtaatctg acccccgtgt ctctgatgtc atcacatggc cctgccttca acacaacgag ccttcgaagg agccttctag gggtggttgc gactacccgg ctgagcacgt cacaaaaccc agaaagttgt ctgtgcccat ttagtataga cagcccaggg ctcttatttc cattcagagt cctaatttgc gagacctggg aacatgctgt actgaggctt gaacacagat gcaaaacagt aacaa ataatagcag. gagttcccca cactgtagcc tcagtccatt tgcacgctca gaaaatctgc tattcctcac tcacctactc acgtgacaaa 7021 7081 7141 6781 6841 6901 6961

Location/Qualifiers

FEATURES

=1G.2B

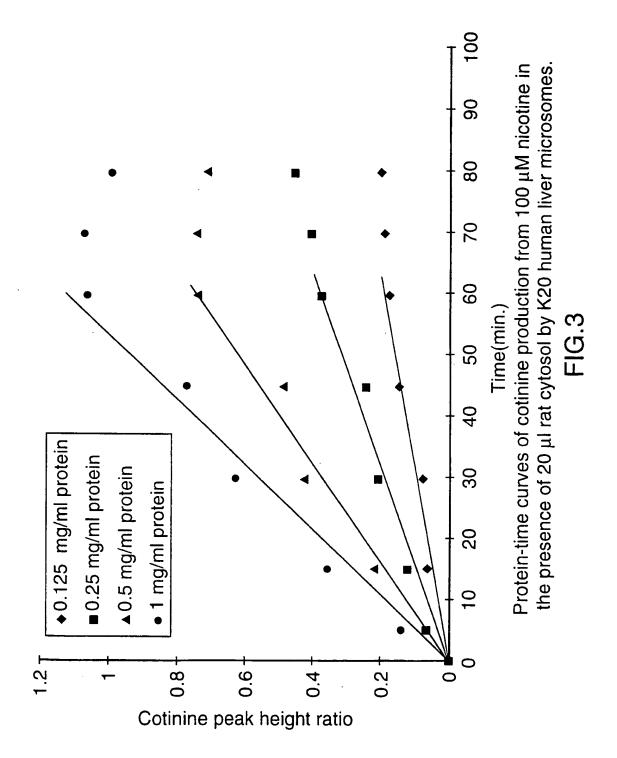
•			•																		
	29-MAY-1992				Chordata;	minidae; Homo.				ancer Research Fund, 🖸			-		P450IIB6 gene				cDNA clones. **map:		J.S.
	HSP452B6 1415 bp RNA Human MRNA FOR CYTOCHROME P-450IIVB6. X13494	•	Cytochrome; cytochrome P450IIB6. human.	Homo sapiens	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;	Vertebrata; Eutheria; Primates; Catarrhini; Ho	1 (bases 1 to 1415)	Miles, J.S.	Direct Submission	Submitted (10-NOV-1988) Miles J.S., Imperial Cancer Research	Lab of Molecular Phrmacology and Drug Metabolism, Hugh Robson	Building, George Square, Edinburgh, EH8 9XD	2 (bases 1 to 1415)			generates a high level of aberrant messages	Nucleic Acids Res. 17 (20), 8241-8255 (1989)	90045947	The sequence is a compilation of genomic and cDNA clones.	chromosomal location=19q12-13.2;	Data kindly reviewed (13-NOV-1989) by Miles,
	LOCUS DEFINITION ACCESSION	NID	KEYWORDS SOHRCE	ORGANISM			REFERENCE	AUTHORS	TITLE	JOURNAL			REFERENCE	AUTHORS	TITLE		JOURNAL	MEDLINE	COMMENT		

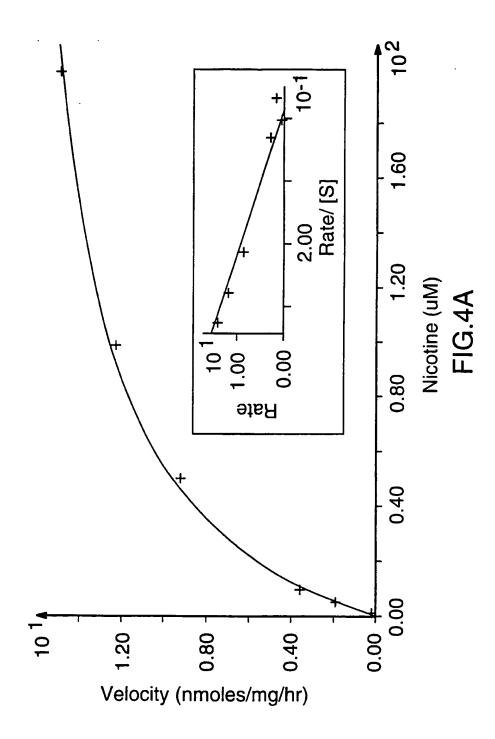
gaatteegee etgeaceeat gaeegeetee caeeagggee eegeeetetg eeettttgg

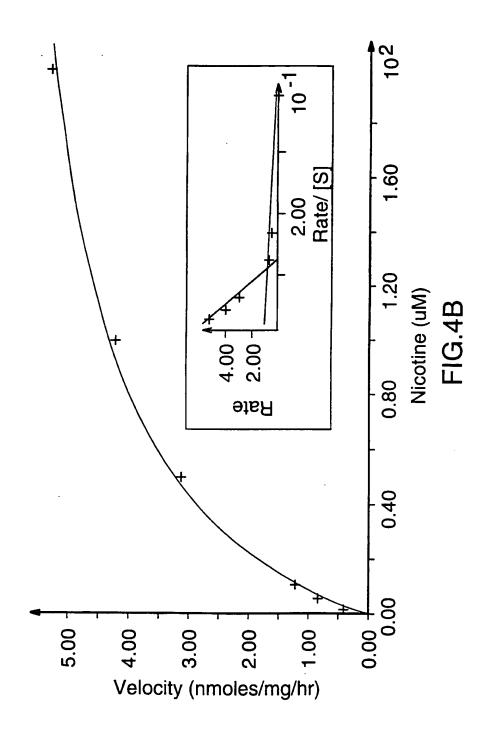
:	រី រ	u.								Н	316 t	
-	omo sapie	1, partial"	2 "	3 "	4 "	5 "	, 9	,, L	8	9", coding	328 g	
11415	/organism="Homo sapiens" 9110	/note=exon 1 111273	/note=exon 274423	/note=exon 3 424584	/note=exon 4 585761	/note=exon 5762903	/note=exon (9041091	/note=exon 7 10921233	/note=exon 8 12341415	/note=exon 9	a 430 c	
source	misc-feature	misc-feature	misc-feature	misc-feature	misc-feature	misc-feature	misc-feature	misc-feature	misc-feature		BASE COUNT 341 a	ORIGIN

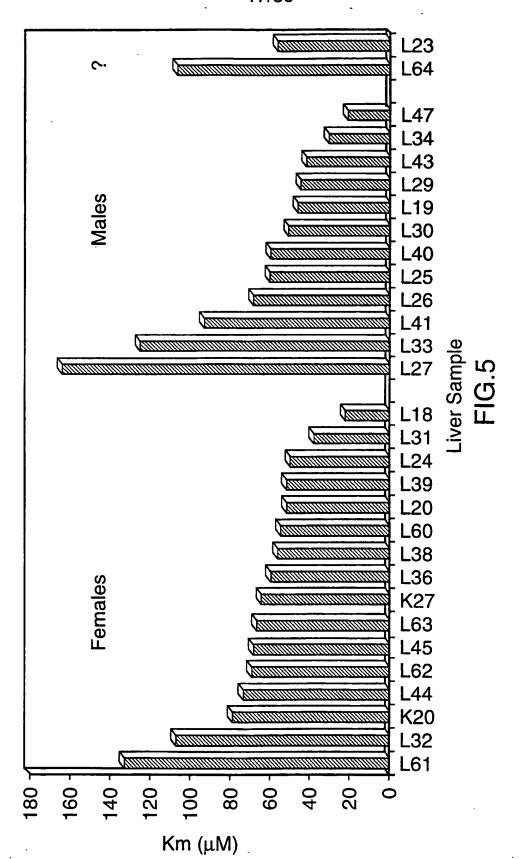
13/59

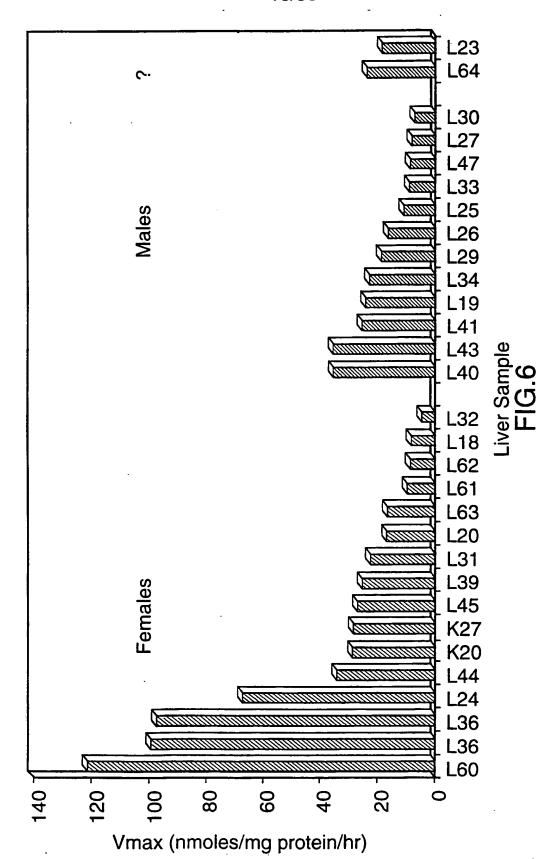
					5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5)
		actaa	ttactacac	ccadatccac	でしたでしてし	~
ggcaaaatac	gtgtggtgtg	cacccagga	atcgatctga	cccagaagac	gccccgtggc	32
tccatggcca	ccagaacttc	ccaccatcct	ctcttcttca	ggaattgttc	tcgcccgagc	26
ggtgaaggca	gatttgtctt	tagggaagcg	cccttctcct	agcttttatc	aaaagactga	1201
ggggcactga	ggatgccaat	accactttct	ttcaatcctg	accagacgcc	actttgaaaa	14
gacccacact	tgctctccat	tcctgagcac	gtatttctca	ggacacagaa	tcatccccaa	∞
cgagggtaca	caccagcttc	tcacccaaca	ccccacattg	catgggtgtg	accttctccc	02
agattttccg	tgagattcag	cagtcatcta	tacacagagg	caaaatgcca	atgaccgagc	9
ccagagcttc	acatcgccct	tgattggccc	attgaacagg	ctacagggag	cagagagagt	0
cctcatgttg	gctcaaatac	tcctgctcat	cgctacggct	caccactctc	agaccaccag	ゼ
gctggcactg	gctcttcttt	acacgctctc	ctcaacctca	ccaccagaac	gtgaattcag	∞
aacgcacaca	agagaaatcc	acatggaaaa	tacctgctcc	catcgacacc	ccaaggacct	\sim
cccagcgccc	aaccctggac	agcaccgtga	agtgtggaga	cattggccac	tcaatgctta	9
ctgcaggaaa	ttacaaaaac	acaggcaagt	cctggggcac	gaaatacttt	ctggcttctt	0
gagctcttct	ccagctgttt	ctgtattcgg	ctcatcagct	gactttttca	tgttctacca	ゼ
atgctgaact	gttcctgaag	aagatcaaga	ttccactacc	tggaaaacga	ccatcgtctt	∞
atcatctgct	taccgccaac	tccagtccat	accttcctct	catggacccc	agggggccct	\sim
cggaaatcca	agaggagctt	agtgtctgat	gaggaggete	gcggattcag	gtgtggagga	9
ggaaagcgga	cttcgggatg	ctatgaggga	tctgtgacca	teggegatte	ggaaggtgct	0
ggaaaccgct	ctttgccaat	atggtgtgat	ttccggggat	cgacccattc	tcgccatggt	T
cggggaaaaa	cttctctggc	aggctgaggc	cttgtggaca	acgggaggcc	tagaggccat	181
ctgtgtggag	cgtggtcatg	gacccaggcc	gtacacctgg	cgtcttcacg	aatatgggga	\sim
ttccgagaga	ctttctgagg	tactcaaatc	agaagaggcc	gcagatggat	gaaaccttct	61



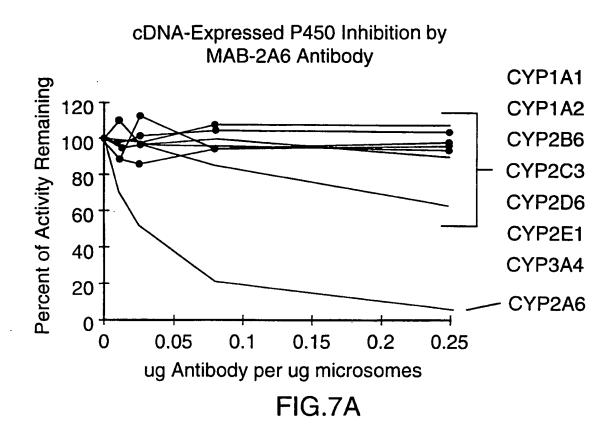


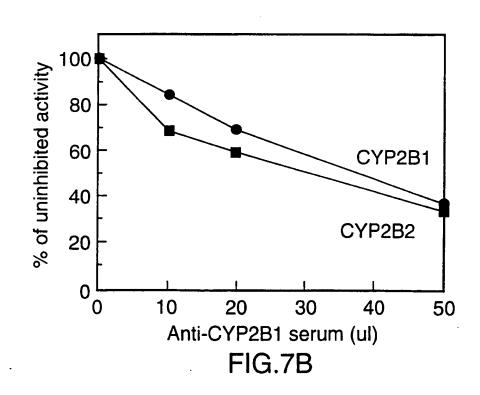






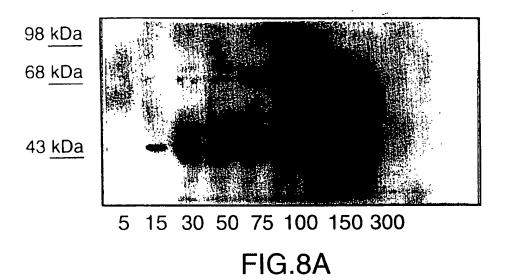
SUBSTITUTE SHEET (RULE 26)

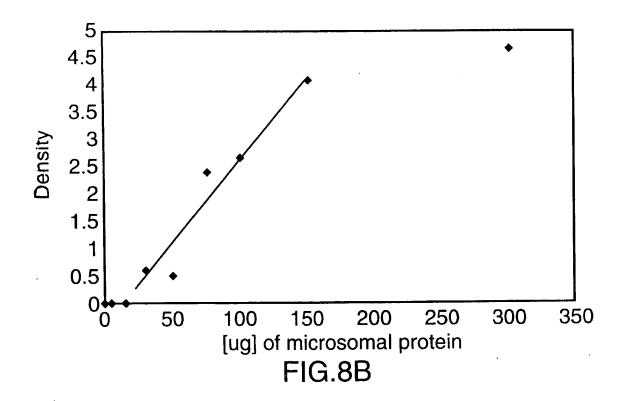


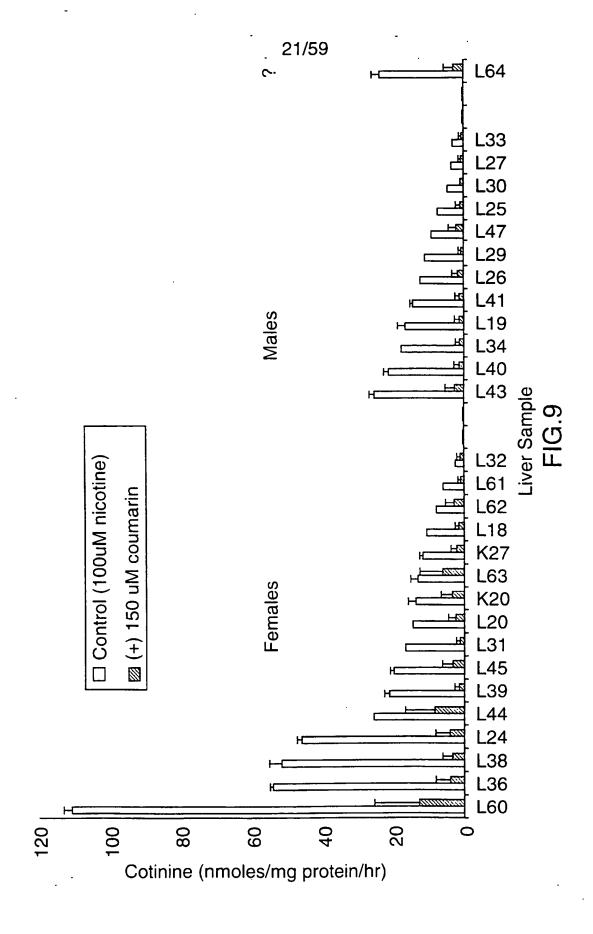


BEST AVAILABLE COPY

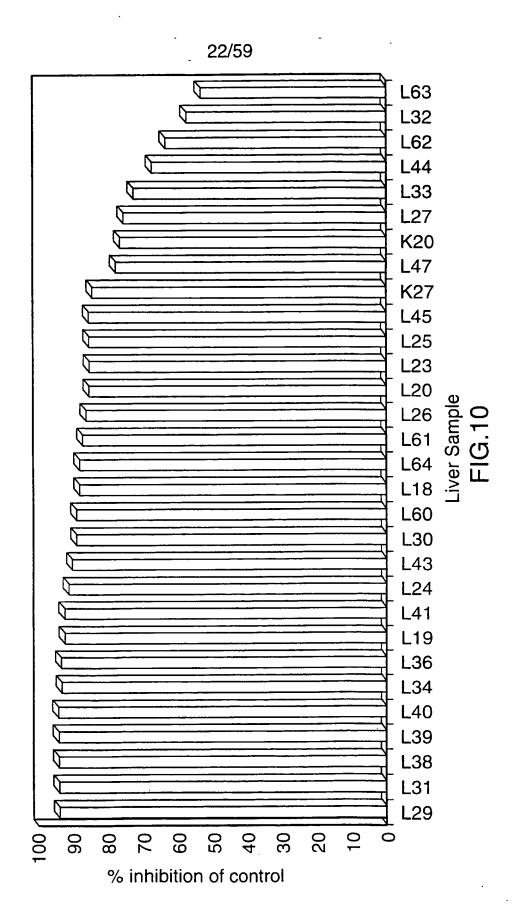
20/59

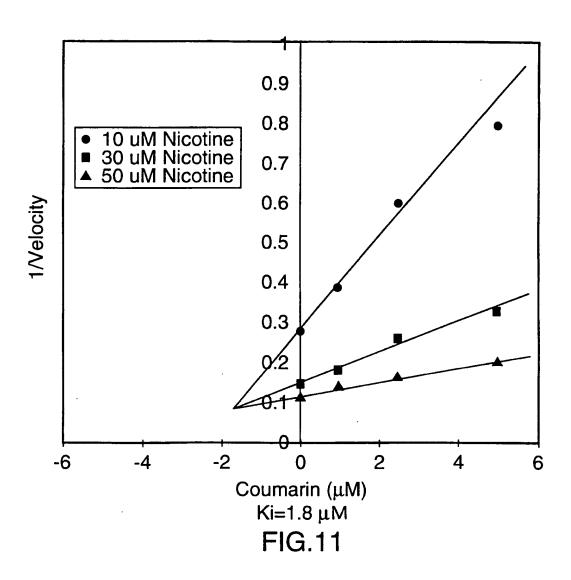




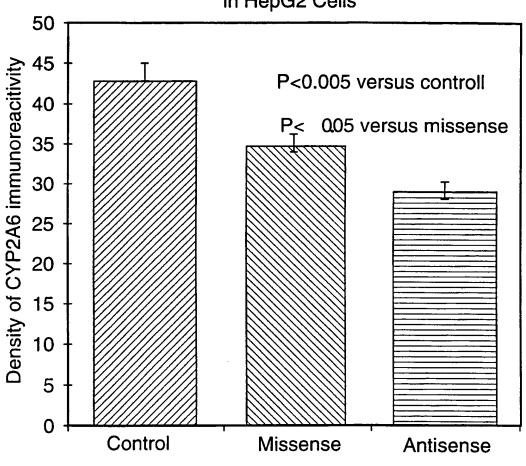


SUBSTITUTE SHEET (RULE 26)



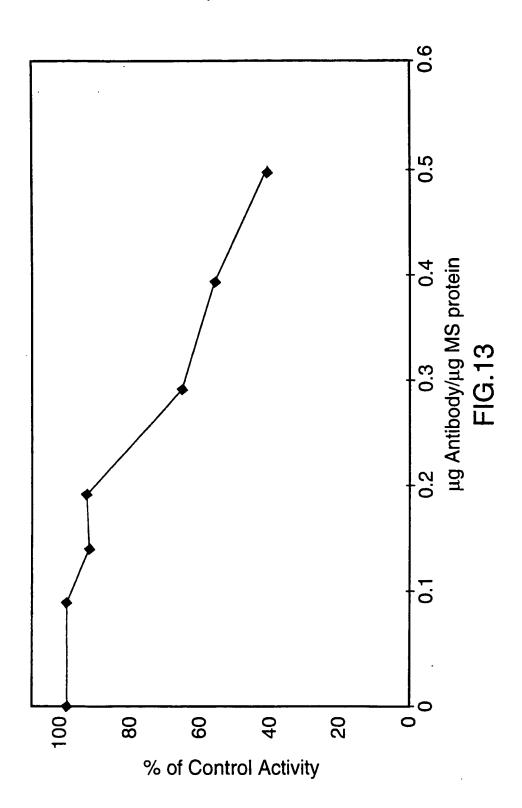


CYP2A6 Antisense Knockdown in HepG2 Cells



Oligodeoxynucleotide Treatment

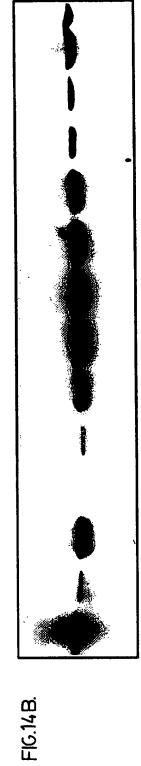
FIG.12



26/59



75 100 30 K20 K27 L18 L19 L20 L23 L24 L25 L26 L27 15

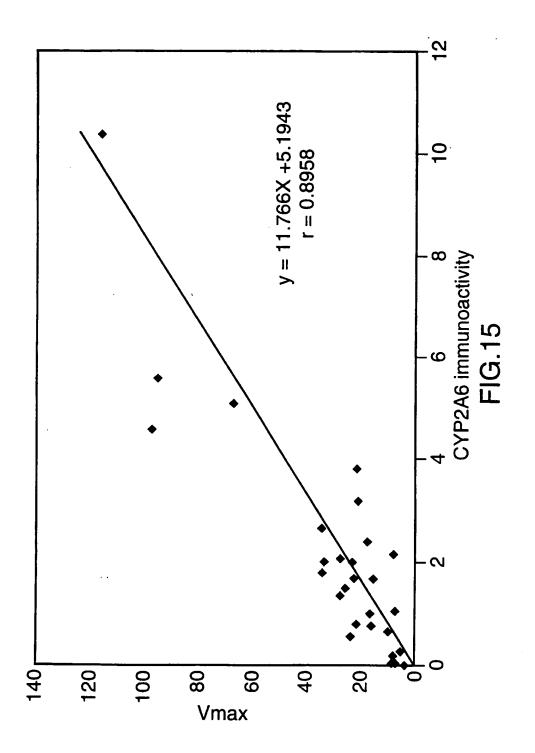


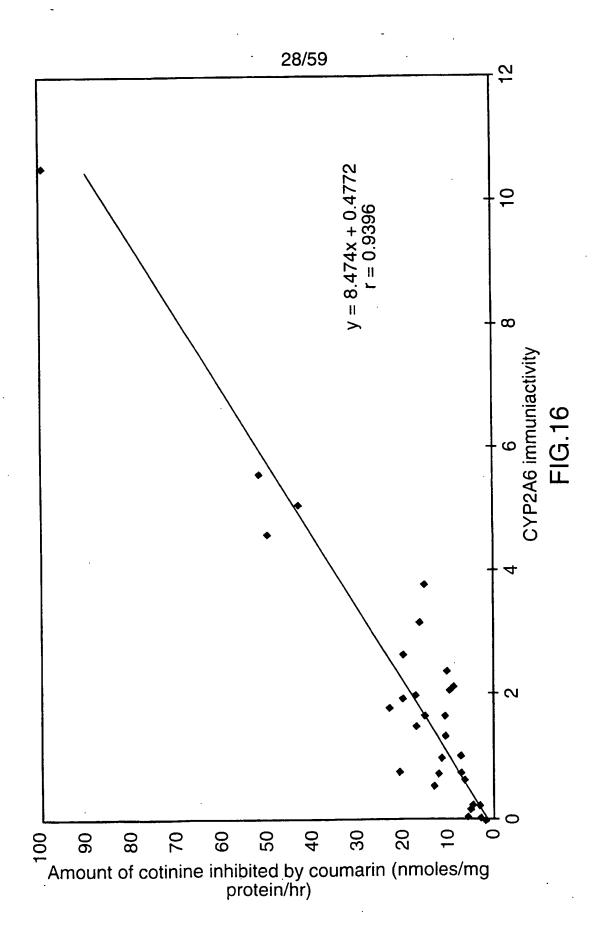
75 100 30 L29 L30 L31 L32 L33 L34 L36 L38 L39 L40 15

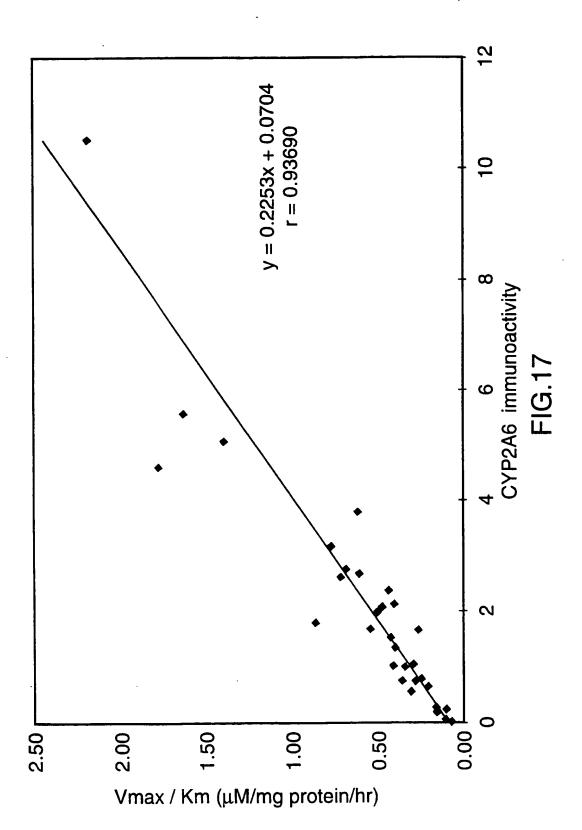


F16.14 C.

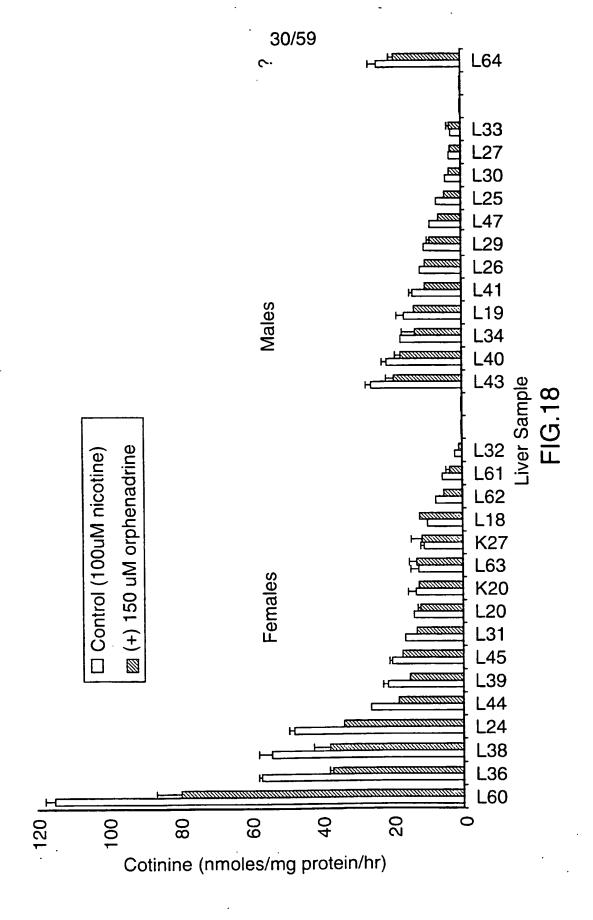
L41 L43 L44 L45 L47 L60 L61 L62 L63 L64



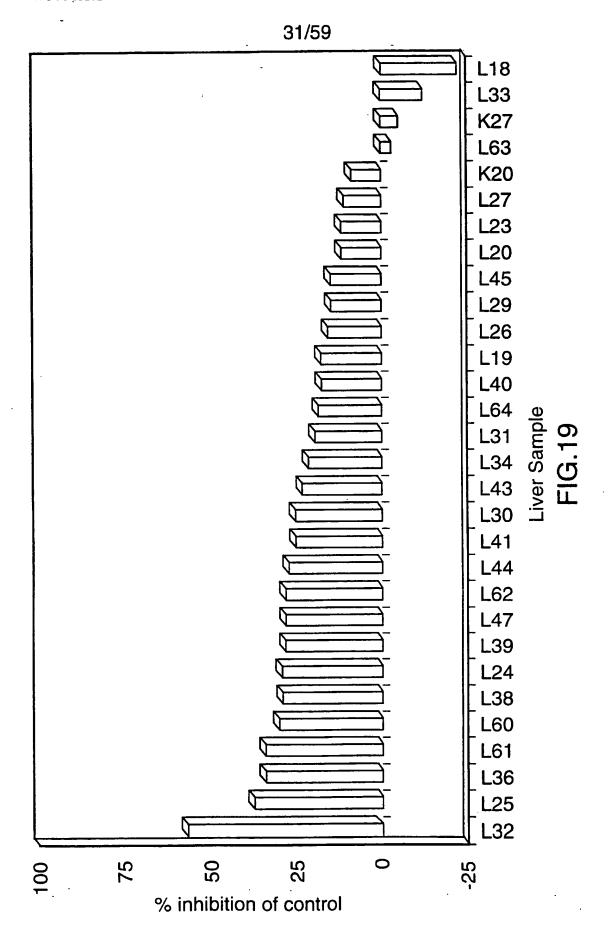




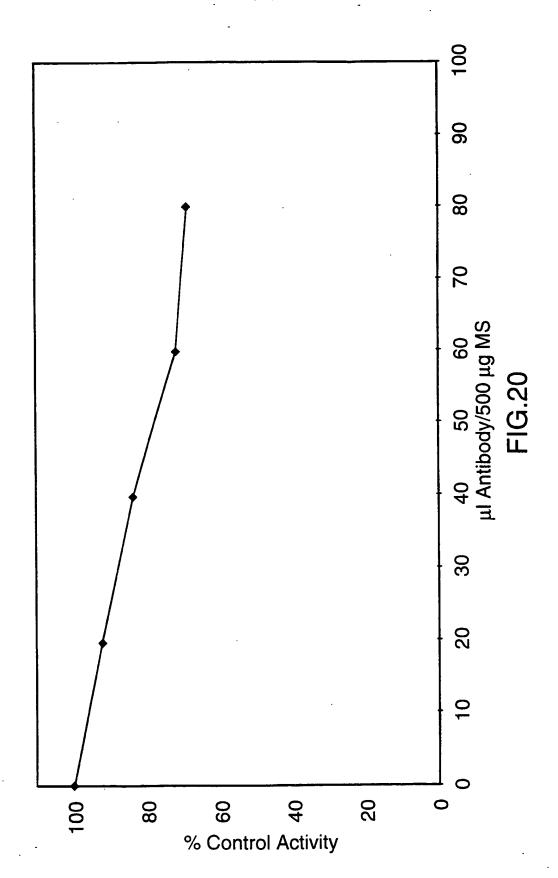
SUBSTITUTE SHEET (RULE 26)



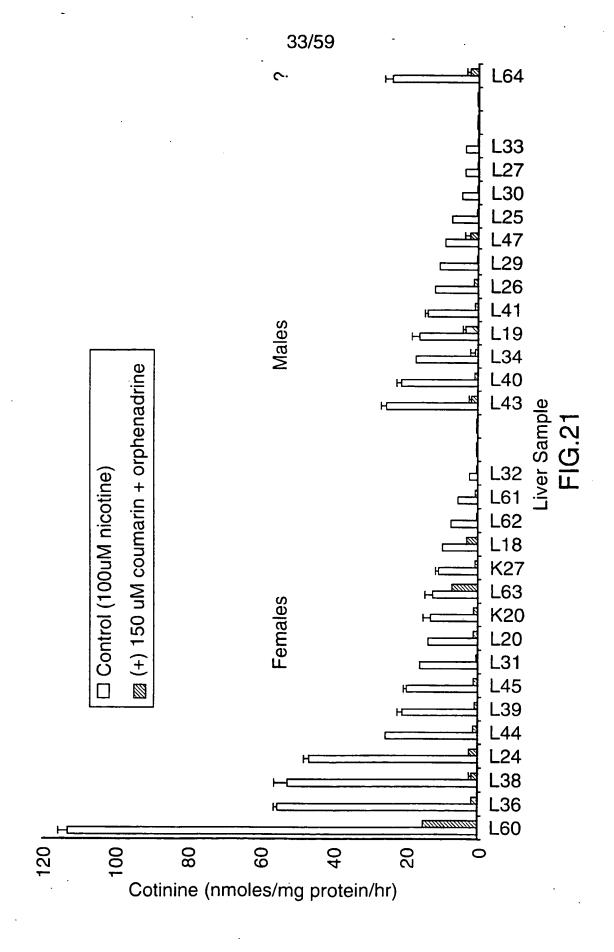
SUBSTITUTE SHEET (RULE 26)

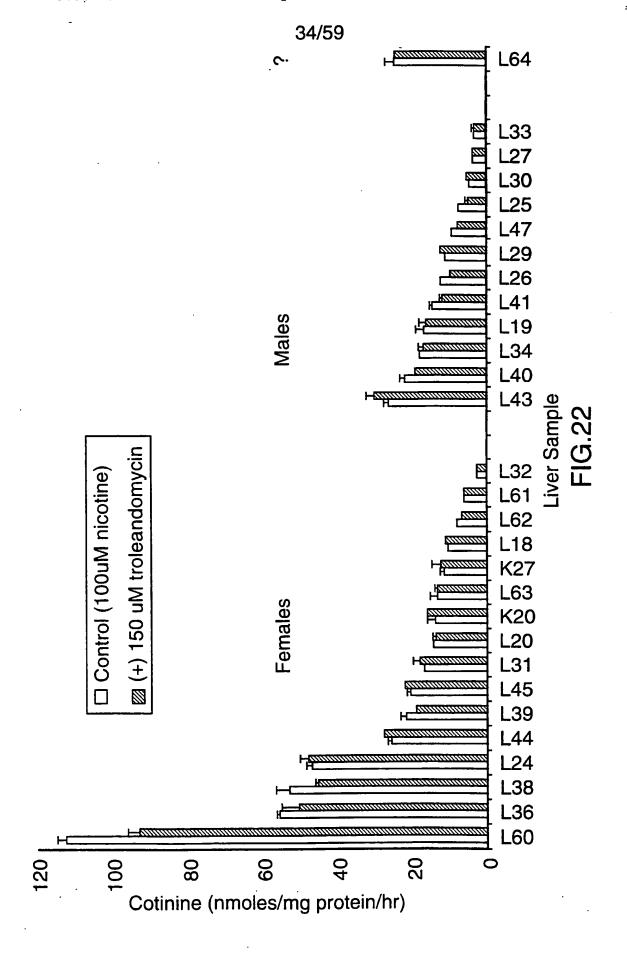


SUBSTITUTE SHEET (RULE 26)



SUBSTITUTE SHEET (RULE 26)





SUBSTITUTE SHEET (RULE 26)

35/59

FIG.23A

SUBSTITUTE SHEET (RULE 26)

36/59

$$C_2H_5$$
 C_1H_1 CH_2 CH_3

Pilocarpine

Nicotine

$$\begin{array}{c|c} \text{CI} & \text{CI} \\ \text{H}_2\text{N} - \begin{array}{c} \text{CH}_2 - \begin{array}{c} \text{CI} \\ \text{NH}_2 \end{array} \end{array}$$

4,4'-Methylene bis[2-chloroaniline

6-Aminochrysene

 α -Naphthoflavone

FIG.23B

About 80% activity left at 0.05 mM concentration

Dicumarol

70% inhibition at 0.5 mM concentration

SM-12502

[(CH₃)₂N]₃P(O)

Hexamethylphosphoramide

(CH₃)₂ NNO

N-Nitrosodimethylamine

FIG.23C

<	ι
7	Ŧ
C	V
	•
C	5
-	_
L	乚

The SAS System Pharmacokinetics of nicotine Experiment BC1;

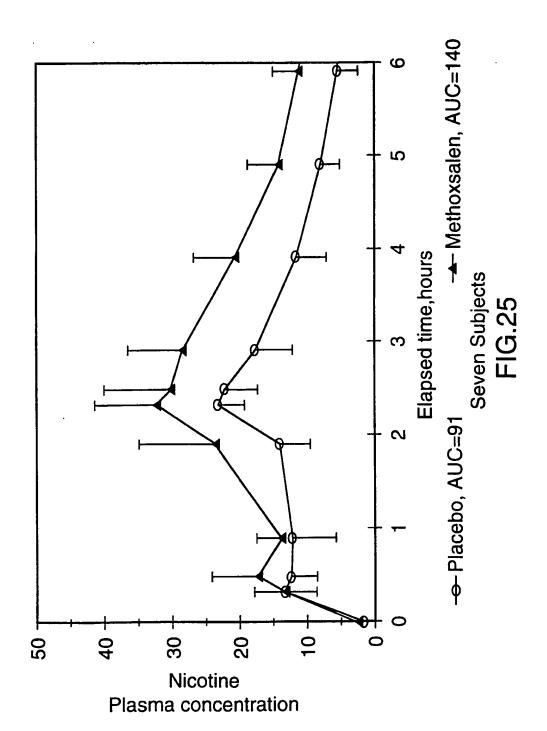
			F Value Pr > F 4.66 0.0397		AUC Mean 90876.07	Value Pr > F 5.43 0.0294 0.09 0.7690			
re-assays	 					ഥ			٠
	COTININE	Mean	Square 151124745	0/06#0#70/0	Root MSE 18001.38	Mean Square 1758023983 30588081	Means	AUC	92354.2010 89397.9447
sed analysis of kinetics based on Does treatment affect AUC?	Compound assayed=COTININE	Jo mnS	od o	12523030000	C.V. 19.80871	Type I SS 10548143898 30588081	Least Squares Me		Methoxsalen10-50 Placebo
Revised analy Do	Соп	AUC	DF 7	13	R-Square 0.844742	DF 6	I	TREATMNT	Methoxs Placebo
K.		Variable:		Total					
	; ; ; ; ;	Dependent	Source Model	Error Corrected		Source SUBJ TREATMNT			

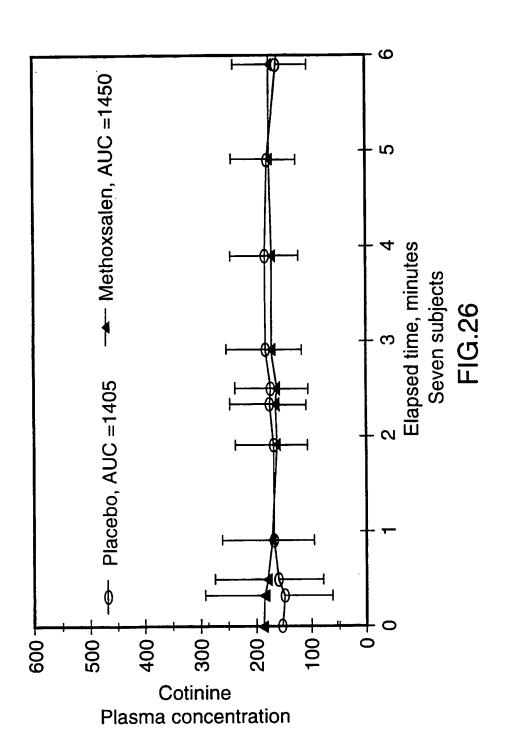
38/59

	L	1
4	∀	۲
C	`	J
	_	3
	1)
	-	-
L	ı	_

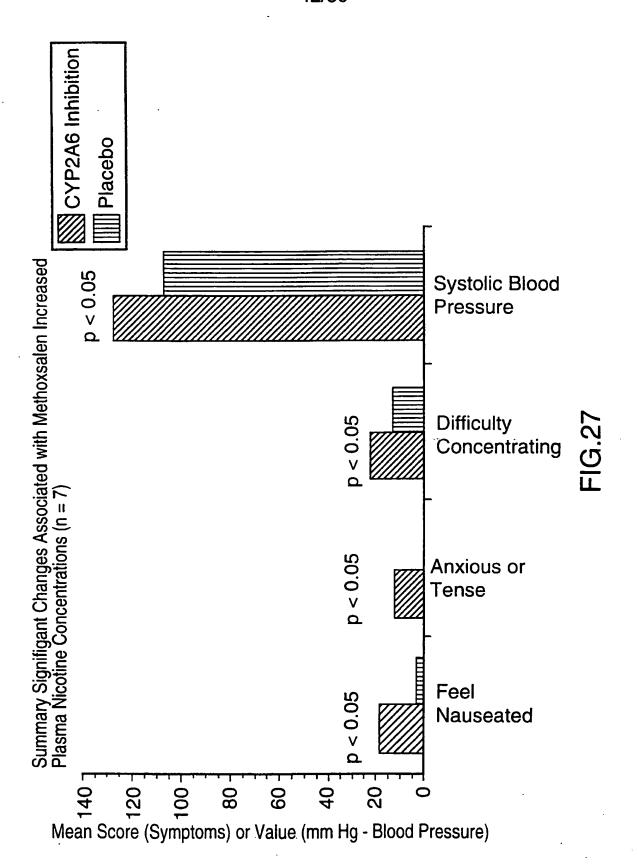
The SAS System Experiment BC1; Pharmacokinetics of nicotine Revised analysis of kinetics based on re-assays Does treatment affect AUC?

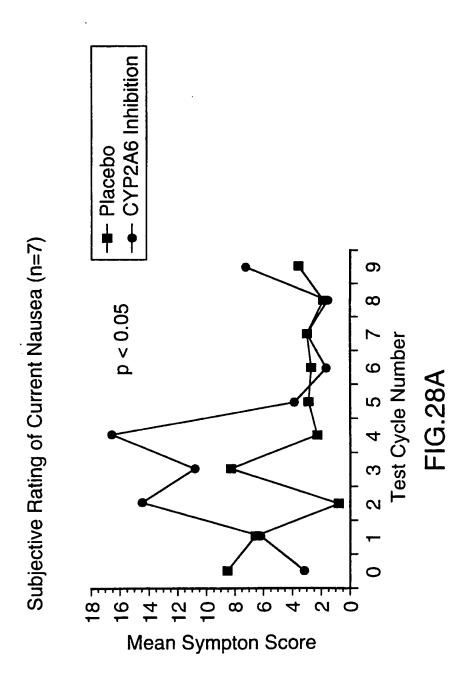
39/59

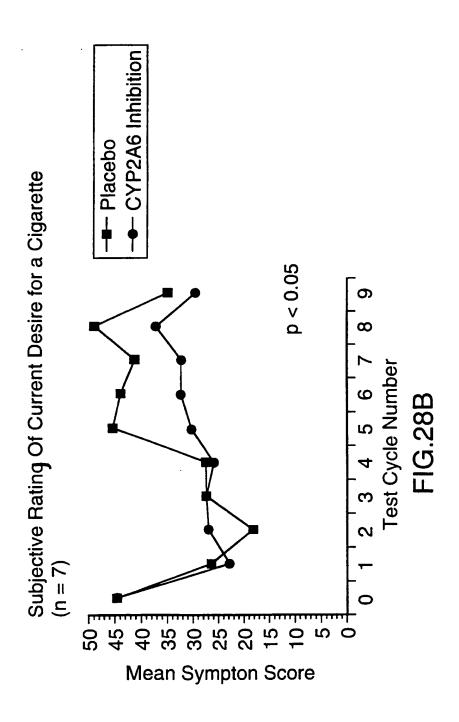


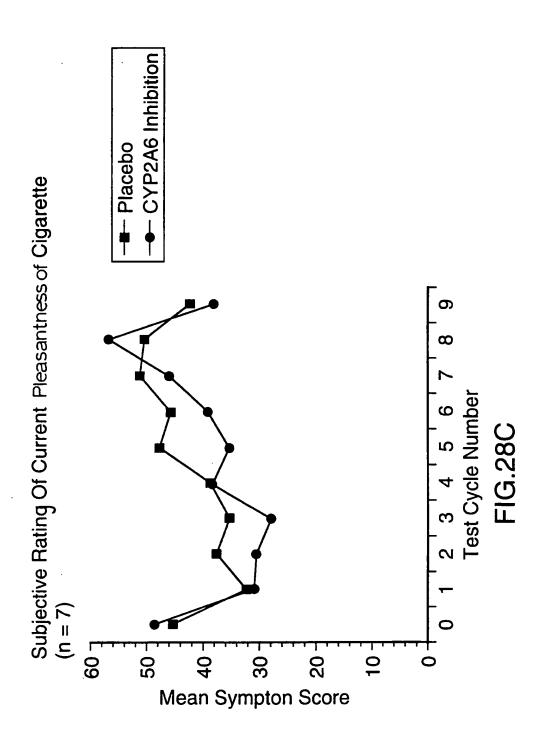


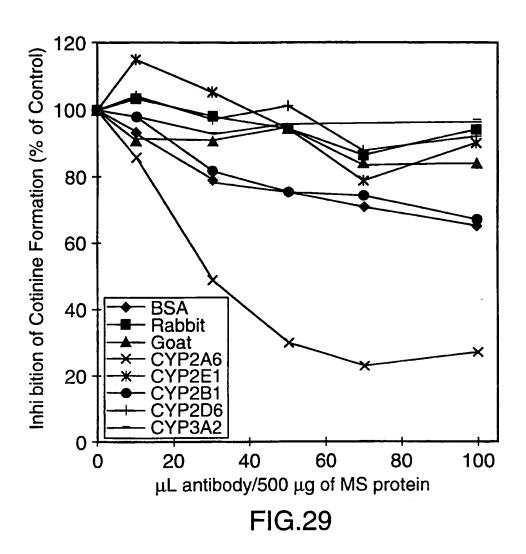
SUBSTITUTE SHEET (RULE 26)











SUBSTITUTE SHEET (RULE 26)

Inhibition of Nicotine to Cotinine Metabolism by various Compounds

Inhibitor	Ŋ	% Inhibition at 10 uM	% Inhibition at 100 uM	% Inhibition at 150 uM	
coumarin	2 uM (n+4)	65 (n=1)	90 (n=1)	85 +/- 11 (SD, n=31)	
7-methoxycoumarin	2.5 uM (n=1)	40 (n=1)	60 (n=3)		
7-methylcoumarin	15 uM⁴	20 (n=1)	70 (n=3)		
7-ethoxycoumarin	>100 uM*	10 (n=1)	20 (n=3)		
7-hydroxycoumarin	200 uM		25 (n+1		•
diethyldithiocarbamic acid	14.5 uM (n=1)				
pilocarpine	0.1 uM				·
naringenin	4.3 uM (n=1)	30 (n=1)	70 (n=3)		
methoxsalen	0.02 uM (n=1)				
naringin	.100 uM*		10 (n=1)		
bupropion		20 (n=1)	30 (n=1)		
orphenadrine	***************************************		***************************************	20 +/- 16 (SD, n=30)	
troleandomycin				3 +/- 11 (SD, n=30)	

all nicotine concentrations were at the Km value for cotinine formation in their respective livers * estimated from screening studies with 10 and 100 uM inhibitor concentrations

FIG.30A

FIG.30B

the CYP2A6 Substrate Coumarin to 7-Hydroxycoumarin Metabolism by various compound		
strate Coumarin to 7-H	Monkey liver	1.69 uM 24.1 uM 0.9 uM
	Human liver	0.29 uM 100.1 uM 0.9 uM
Ki Values for the Inhibition of	Inhibitor	methoxsalen nicotine pilocarpine

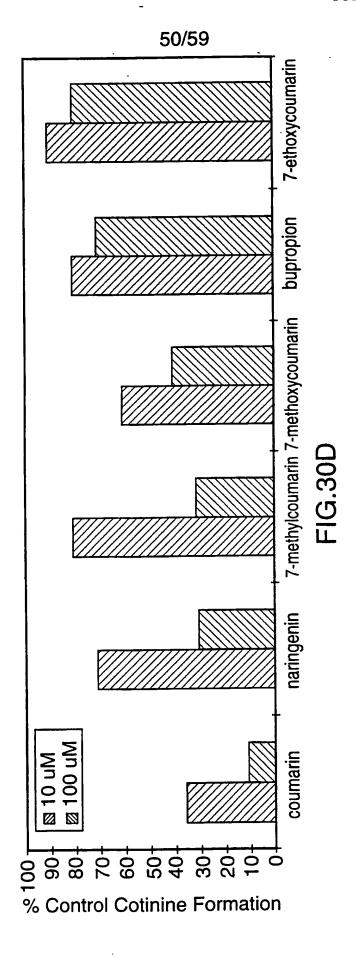
SUBSTITUTE SHEET (RULE 26)

49/59

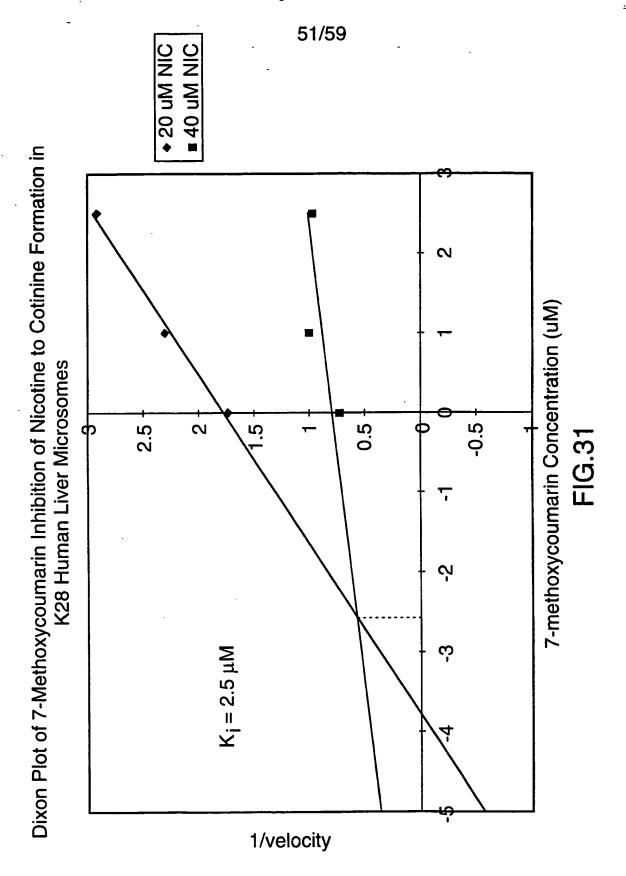
Effect of Various Compounds on Cotinine Formation % control cotinine formation

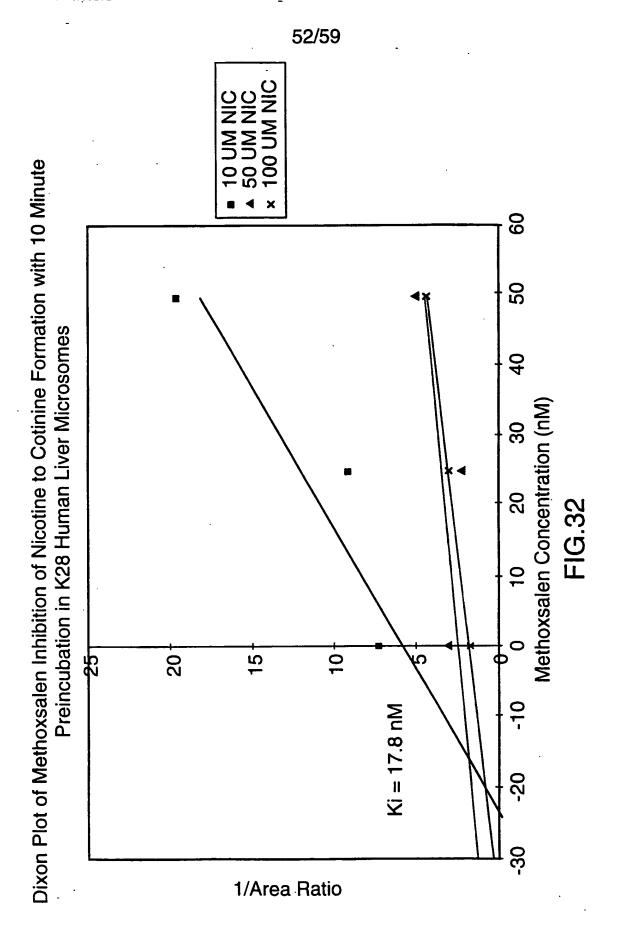
Inhibitor	10 uM	100 uM
coumarin	35	10
naringenin	70	30
7-methylcoumarin	80	30
7-methoxycoumarin	60	40
bupropion	80	70
7-ethoxycoumarin	90	80

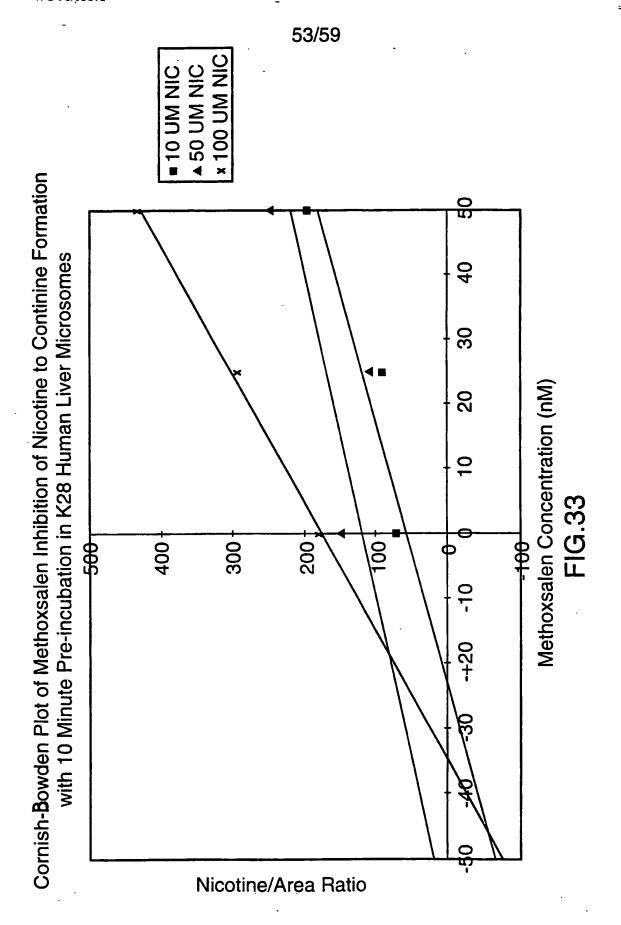
FIG.30C

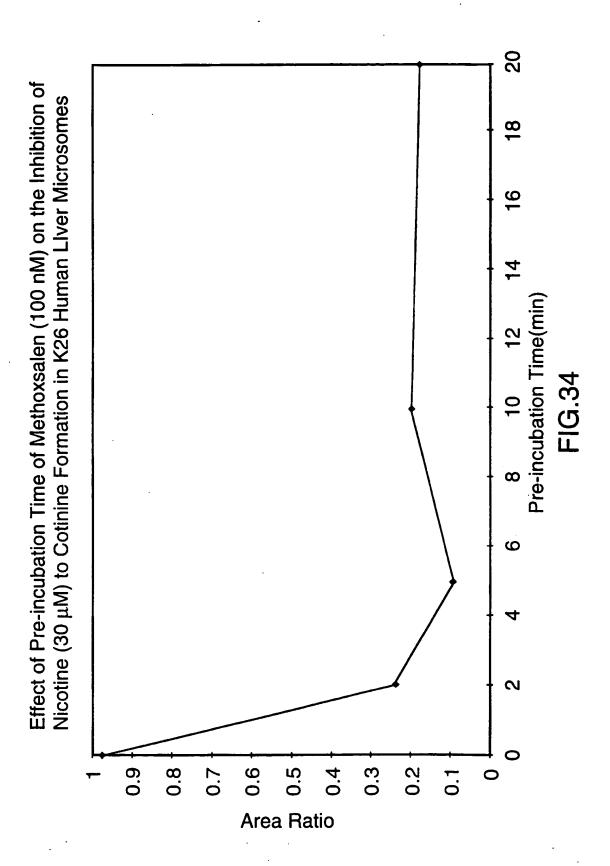


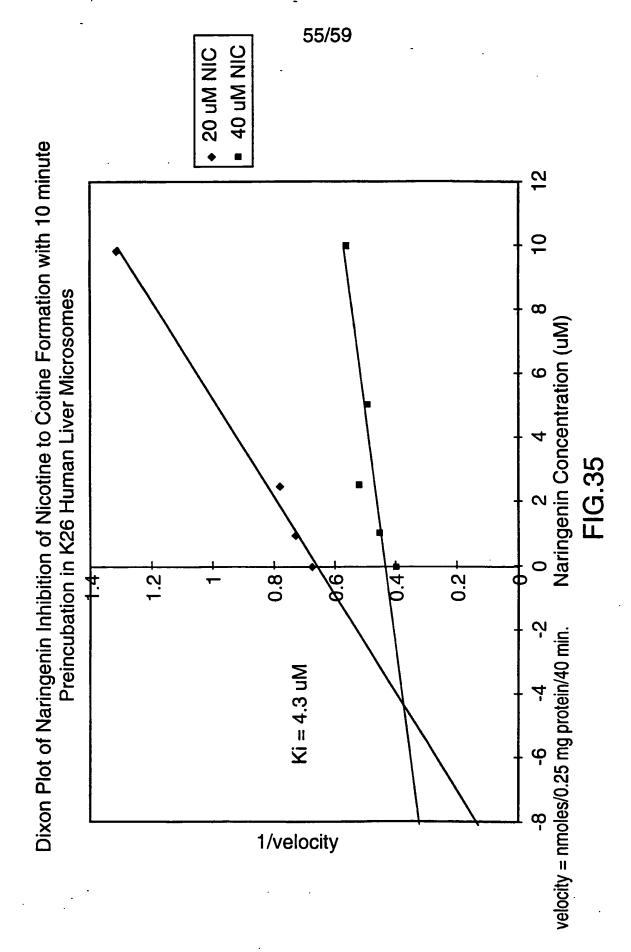
SUBSTITUTE SHEET (RULE 26)

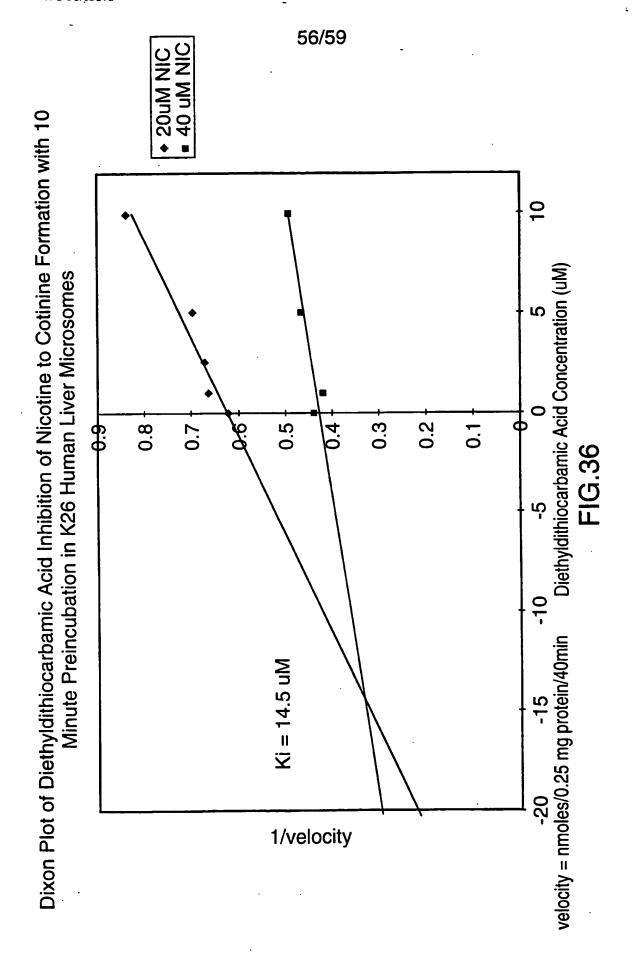












Comparsison Between Morning and Afternoon Testing Sessions

